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## An Integrative Approach to Generating a Reference Transcriptome for Sugarcane

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The sugarcane industry is a substantial agricultural activity in South Africa, which contributes significantly to the country's gross domestic product and positively impacts on the lives of over a million people. Economic loss due to *Eldana saccharina*, a lepidopteran stem-borer, is estimated to be R900 million per annum. A better understanding of the molecular mechanisms involved in resistance against eldana would be an important step towards targeted breeding of resistant sugarcane varieties. In a genomic context, sugarcane is classed as an 'orphan crop' as no genome assembly is currently available. However, next generation sequencing (NGS) technologies have enabled large scale sequencing of genomes and transcriptomes providing the data needed to uncover these mechanisms. Commercial sugarcane cultivars (*Saccharum* spp. hybrids) have large and complex polyploid genomes. Moreover, it is not known how gene expression is influenced by the multiple alleles created due to the aneuploid and polyploid nature of the genome. Our aim is to harness the wealth of in-house and publicly available genomic and transcriptomic data in order to construct a reference transcriptome for use in sugarcane RNA-seq studies, whilst overcoming the limitations of *de novo* transcriptome assembly with low coverage data. Not only will this project endeavour to uncover the molecular mechanisms underpinning resistance to eldana, but the approach taken should allow the development of a generic and modular analysis pipeline capable of creating reference transcriptomes, in the absence of a reference genome, in other non-model plant species.

### HPC content

This project makes use of high throughput computing to deal with large genomic and transcriptomic datasets. Annotation and assembly is a computationally intensive process that requires considerable CPU time and effort. Bioinformatic tools used for this task include assemblers such as Trinity, mira and SPAdes, and various aligners including bowtie2, blast and exonerate.

**Primary author:** Ms JACOB, Robyn (South African Sugarcane Research Institute)

**Co-author:** Dr LLOYD EVANS, Dyfed (South African Sugarcane Research Institute, UKZN)

**Presenter:** Ms JACOB, Robyn (South African Sugarcane Research Institute)

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